

Archived Editions (COVID-19 Genomics and Precision Public Health Weekly Update)

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COVID-19 Genomics and Precision Public Health Weekly Update Content

- Pathogen and Human Genomics Studies
- Non-Genomics Precision Health Studies
- News, Reviews and Commentaries

Pathogen and Human Genomics Studies

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Health care workers with prior SARS-CoV-2 infection followed by 2 doses of mRNA vaccine (3 independent exposures to spike antigen) developed higher spike antibody measurements than individuals with vaccination alone. Consistent with work comparing extended vaccine dosing intervals, the study showed that a longer interval between infection and first vaccine dose may enhance the antibody response.

- Highly-Sensitive Lineage Discrimination of SARS-CoV-2 Variants through Allele-Specific Probe Polymerase Chain Reaction (<https://www.medrxiv.org/content/10.1101/2021.11.01.21265384v1>)
JD Radcliff et al, MEDRXIV, November 2, 2021

Although next-generation sequencing (NGS) has been adopted as the gold standard method for discriminating SARS-CoV-2 lineages, alternative methods may be required when processing samples with low viral loads or low RNA quality. An allele-specific probe polymerase chain reaction (ASP-PCR) targeting lineage-specific single nucleotide polymorphisms (SNPs) was developed and used to screen 1,082 samples from two clinical trials in the United Kingdom and Brazil.

- Equipment-free detection of SARS-CoV-2 and Variants of Concern using Cas13 (<https://www.medrxiv.org/content/10.1101/2021.11.01.21265764v1>)
JA Sanz et al, MEDRXIV, November 2, 2021

Here, we develop SHINEv2, a Cas13-based nucleic acid diagnostic that combines quick and ambient temperature sample processing and lyophilized reagents to greatly simplify the test procedure and assay distribution. We benchmarked a SHINEv2 assay for SARS-CoV-2 detection against state-of-the-art antigen-capture tests using 96 patient samples, demonstrating 50-fold greater sensitivity and 100% specificity. We designed SHINEv2 assays for discriminating the Alpha, Beta, Gamma and Delta VOCs, which can be read out visually using lateral flow technology. We further demonstrate that our assays can be performed without any equipment in less than 90 minutes.

- Viral loads of Delta-variant SARS-CoV-2 breakthrough infections after vaccination and booster with BNT162b2 (<https://www.nature.com/articles/s41591-021-01575-4>)
ML Tiefenbrun et al, Nature Medicine, November 2, 2021

By analyzing viral loads of over 16,000 infections during the current, Delta-variant-dominated pandemic wave in Israel, we found that BTIs in recently fully vaccinated individuals have lower viral loads than infections in unvaccinated individuals. However, this effect starts to decline 2 months after vaccination and ultimately vanishes 6 months or longer after vaccination. Notably, we found that the effect of BNT162b2 on reducing BTI viral loads is restored after a booster dose. These results suggest

that BNT162b2 might decrease the infectiousness of BTIs even with the Delta variant, and that, although this protective effect declines with time, it can be restored, at least temporarily, with a third, booster, vaccine dose.

- BNT162b2 and mRNA-1273 COVID-19 vaccine effectiveness against the SARS-CoV-2 Delta variant in Qatar (<https://www.nature.com/articles/s41591-021-01583-4>)

NP Tang et al, Nature Medicine, November 2, 2021

With the global expansion of the highly transmissible SARS-CoV-2 Delta (B.1.617.2) variant, we conducted a matched test-negative case-control study to assess the real-world effectiveness of COVID-19 messenger RNA vaccines against infection with Delta in Qatar's population. Our findings show robust effectiveness for both BNT162b2 and mRNA-1273 in preventing Delta hospitalization and death in Qatar's population, despite lower effectiveness in preventing infection, particularly for the BNT162b2 vaccine.

- SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a wide variety of tiss ([https://www.cell.com/cell-reports/fulltext/S2211-1247\(21\)01502-3](https://www.cell.com/cell-reports/fulltext/S2211-1247(21)01502-3))

M d'Antonio et al, Cell Reports, November 2, 2021

Highlights: Identification of 23 genomic loci with suggestive associations for COVID-19 disease. Colocalized GWAS & eQTL signals associate with expression of 20 genes in 62 tissues. 45% of GWAS signals do not colocalize with eQTLs in blood or lung. Genetic fine mapping identifies putative causal variants at COVID-19 GWAS loci.

- Phase 3 Trial of mRNA-1273 during the Delta-Variant Surge (https://www.nejm.org/doi/full/10.1056/NEJMc2115597?query=featured_home)

LR Baden et al, NEJM, November 3, 2021

Overall, incidence rates of Covid-19 were lower among participants in the mRNA-1273p group (who had been vaccinated more recently) than among those in the mRNA-1273e group during July and August 2021, when the delta variant was dominant. The difference appears to have been driven by disease in younger participants, which indicates the presence of potential confounding behavioral factors in these participants that may have led to a higher exposure to the virus.

- Neutralization of the SARS-CoV-2 Mu Variant by Convalescent and Vaccine Serum (https://www.nejm.org/doi/full/10.1056/NEJMc2114706?query=featured_home)

K Uriu et al, NEJM, November 3, 2021

Although the beta variant (a variant of concern) was thought to be the most resistant variant to date,^{3,4} the mu variant was 2.0 as resistant to neutralization by convalescent serum and 1.5 times as resistant to neutralization by vaccine serum as the beta variant. Thus, the mu variant shows a pronounced resistance to antibodies elicited by natural SARS-CoV-2 infection and by the BNT162b2 mRNA vaccine.

- An oral SARS-CoV-2 Mpro inhibitor clinical candidate for the treatment of COVID-19 (<https://www.science.org/doi/10.1126/science.abl4784>)

DR Owen et al, Science, November 2, 2021

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